



#2

OIKE

RAW SEQUENCE LISTING

DATE: 02/25/2002

PATENT APPLICATION: US/10/067,291

TIME: 11:54:03

Input Set : N:\Crf3\RULE60\10067291.txt

Output Set: N:\CRF3\02252002\J067291.raw

3 <110> APPLICANT: Takashima, Yoshiki
 4 Mitsuda, Satoshi
 6 <120> TITLE OF INVENTION: Protein capable of catalyzing transamination
 7 stereoselectively, gene encoding said protein
 8 and use thereof
 10 <130> FILE REFERENCE: Q58251
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/067,291
 13 <141> CURRENT FILING DATE: 2002-02-07
 15 <150> PRIOR APPLICATION NUMBER: 09/527,522
 16 <151> PRIOR FILING DATE: 2000-03-16
 19 <150> PRIOR APPLICATION NUMBER: JP 11/075511
 20 <151> PRIOR FILING DATE: 1999-03-19
 22 <150> PRIOR APPLICATION NUMBER: JP 11/088634
 23 <151> PRIOR FILING DATE: 1999-03-30
 25 <160> NUMBER OF SEQ ID NOS: 12
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 339
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Mycobacterium aurum
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: SC-S423
 37 <400> SEQUENCE: 1
 38 Met Thr Ala Leu Ser Asp Leu Gly Thr Ser Asn Leu Val Ala Val Glu
 39 1 5 10 15
 41 Pro Gly Ala Ile Arg Glu Asp Thr Pro Ala Gly Ser Val Ile Gln Tyr
 42 20 25 30
 44 Ser Asp Tyr Glu Leu Asp Thr Ser Ser Pro Phe Ala Gly Gly Val Ala
 45 35 40 45
 47 Trp Ile Glu Gly Glu Tyr Leu Pro Ala Glu Glu Ala Lys Ile Ser Ile
 48 50 55 60
 50 Phe Asp Thr Gly Phe Gly His Ser Asp Leu Thr Tyr Thr Val Ala His
 51 65 70 75 80
 53 Val Trp His Gly Asn Ile Phe Arg Leu Gly Asp His Leu Asp Arg Leu
 54 85 90 95
 56 Leu Asp Gly Ala Ser Lys Leu Arg Leu Asp Ala Gly Tyr Ser Lys Asp
 57 100 105 110
 59 Glu Leu Ala Glu Ile Thr Lys Lys Cys Val Ser Met Ser Gln Leu Arg
 60 115 120 125
 62 Glu Ser Phe Val Asn Leu Thr Val Thr Arg Gly Tyr Gly Lys Arg Lys
 63 130 135 140
 65 Gly Glu Lys Asp Leu Ser Lys Leu Thr His Gln Val Tyr Ile Tyr Ala
 66 145 150 155 160

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68 Ile Pro Tyr Leu Trp Ala Phe Pro Pro Ala Glu Gln Ile Phe Gly Thr
69           165           170           175
71 Thr Ala Ile Val Pro Arg His Val Arg Arg Ala Gly Arg Asn Thr Val
72           180           185           190
74 Asp Pro Thr Ile Lys Asn Tyr Gln Trp Gly Asp Leu Thr Ala Ala Ser
75           195           200           205
77 Phe Glu Ala Lys Asp Arg Gly Ala Arg Thr Ala Ile Leu Leu Asp Ser
78           210           215           220
80 Asp Asn Cys Val Ala Glu Gly Pro Gly Phe Asn Val Cys Ile Val Lys
81 225           230           235           240
83 Asp Gly Lys Leu Ala Ser Pro Ser Arg Asn Ala Leu Pro Gly Ile Thr
84           245           250           255
86 Arg Lys Thr Val Phe Glu Leu Ala Asp Gln Met Gly Ile Glu Ala Thr
87           260           265           270
89 Leu Arg Asp Val Thr Ser Arg Glu Leu Tyr Asp Ala Asp Glu Leu Met
90           275           280           285
92 Ala Val Thr Thr Ala Gly Gly Val Thr Pro Ile Asn Ser Leu Asp Gly
93           290           295           300
95 Glu Ala Val Gly Asn Gly Glu Pro Gly Pro Leu Thr Val Ala Ile Arg
96 305           310           315           320
98 Asp Arg Phe Trp Ala Leu Met Asp Glu Pro Gly Pro Leu Ile Glu Thr
99           325           330           335
101 Ile Glu Tyr
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 1020
106 <212> TYPE: DNA
107 <213> ORGANISM: Mycobacterium aurum
109 <220> FEATURE:
110 <223> OTHER INFORMATION: SC-S423
112 <220> FEATURE:
113 <221> NAME/KEY: CDS
114 <222> LOCATION: (1)..(1017)
116 <400> SEQUENCE: 2
117 atg act gct ctt tca gac ctc ggc acc tcc aac ctg gtg gcc gtc gag 48
118 Met Thr Ala Leu Ser Asp Leu Gly Thr Ser Asn Leu Val Ala Val Glu
119 1 5 10 15
121 ccc ggc gcc atc cgc gag gac acc ccg gcc ggc tcg gtg atc cag tac 96
122 Pro Gly Ala Ile Arg Glu Asp Thr Pro Ala Gly Ser Val Ile Gln Tyr
123 20 25 30
125 agc gac tac gaa ctg gac acc tcc agc ccg ttc gcc ggc gtc gtc gcc 144
126 Ser Asp Tyr Glu Leu Asp Thr Ser Ser Pro Phe Ala Gly Gly Val Ala
127 35 40 45
129 tgg atc gag ggc gaa tac ctg ccg gcc gaa gaa gcg aag atc tcc atc 192
130 Trp Ile Glu Gly Glu Tyr Leu Pro Ala Glu Glu Ala Lys Ile Ser Ile
131 50 55 60
133 ttc gac acc gga ttc ggt cat tcc gat ctg acc tac acc gtc gcg cat 240
134 Phe Asp Thr Gly Phe Gly His Ser Asp Leu Thr Tyr Thr Val Ala His
135 65 70 75 80
137 gta tgg cac ggc aac atc ttc cgg ctc ggc gac cac ctg gac cgg ttg 288

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138 Val Trp His Gly Asn Ile Phe Arg Leu Gly Asp His Leu Asp Arg Leu
139                               85                               90                               95
141 ctc gac ggg gcg tcc aag ctg cgc ctg gac gcc ggg tac agc aag gac 336
142 Leu Asp Gly Ala Ser Lys Leu Arg Leu Asp Ala Gly Tyr Ser Lys Asp
143                               100                               105                               110
145 gaa ctg gcc gag atc acc aag aag tgc gtg tcg atg tcg cag ctg cgc 384
146 Glu Leu Ala Glu Ile Thr Lys Lys Cys Val Ser Met Ser Gln Leu Arg
147                               115                               120                               125
149 gaa tcg ttc gtg aat ctg acc gtc acc cgg gga tac gga aag cgc aag 432
150 Glu Ser Phe Val Asn Leu Thr Val Thr Arg Gly Tyr Gly Lys Arg Lys
151                               130                               135                               140
153 ggc gag aag gac ctg tcc aag ctc acc cat cag gtg tac atc tac gcc 480
154 Gly Glu Lys Asp Leu Ser Lys Leu Thr His Gln Val Tyr Ile Tyr Ala
155 145                               150                               155                               160
157 atc ccg tac ctg tgg gcc ttc ccg ccc gcc gag cag atc ttc ggc acc 528
158 Ile Pro Tyr Leu Trp Ala Phe Pro Pro Ala Glu Gln Ile Phe Gly Thr
159                               165                               170                               175
161 acc gcg atc gtg ccg cgc cat gtc cgc cgc gcc ggc cgc aac acc gtc 576
162 Thr Ala Ile Val Pro Arg His Val Arg Arg Ala Gly Arg Asn Thr Val
163                               180                               185                               190
165 gac ccg acc atc aag aac tac cag tgg ggt gat ctc acc gca gcc agt 624
166 Asp Pro Thr Ile Lys Asn Tyr Gln Trp Gly Asp Leu Thr Ala Ala Ser
167                               195                               200                               205
169 ttc gaa gcc aag gac cgt ggt gcg cgc acc gcg atc ctg ctc gac tcg 672
170 Phe Glu Ala Lys Asp Arg Gly Ala Arg Thr Ala Ile Leu Leu Asp Ser
171                               210                               215                               220
173 gac aac tgc gtg gcc gaa ggt ccg ggc ttc aac gtg tgc atc gtc aag 720
174 Asp Asn Cys Val Ala Glu Gly Pro Gly Phe Asn Val Cys Ile Val Lys
175 225                               230                               235                               240
177 gac ggc aag ctg gcc tcc ccg tcc ccg aac gcg ttg ccg ggc atc acc 768
178 Asp Gly Lys Leu Ala Ser Pro Ser Arg Asn Ala Leu Pro Gly Ile Thr
179                               245                               250                               255
181 cgt aag acg gtg ttc gaa ctg gcc gac cag atg ggc atc gaa gcc acc 816
182 Arg Lys Thr Val Phe Glu Leu Ala Asp Gln Met Gly Ile Glu Ala Thr
183                               260                               265                               270
185 ctg cgc gac gtc acc agc cgt gaa ctc tac gac gcc gac gag ttg atg 864
186 Leu Arg Asp Val Thr Ser Arg Glu Leu Tyr Asp Ala Asp Glu Leu Met
187                               275                               280                               285
189 gcg gtc acc acc gcg ggc ggg gtc aca ccg atc aac tcg ctg gat ggc 912
190 Ala Val Thr Thr Ala Gly Gly Val Thr Pro Ile Asn Ser Leu Asp Gly
191                               290                               295                               300
193 gag gcc gtg ggc aac ggc gag ccc ggt cca ctg acg gtg gcc atc cgg 960
194 Glu Ala Val Gly Asn Gly Glu Pro Gly Pro Leu Thr Val Ala Ile Arg
195 305                               310                               315                               320
197 gac ccg ttc tgg gcg ctg atg gac gag ccg ggc ccg ctg atc gaa acg 1008
198 Asp Arg Phe Trp Ala Leu Met Asp Glu Pro Gly Pro Leu Ile Glu Thr
199                               325                               330                               335
201 atc gaa tac tga 1020
202 Ile Glu Tyr

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Input Set : N:\Crf3\RULE60\10067291.txt

Output Set: N:\CRF3\02252002\J067291.raw

205 <210> SEQ ID NO: 3
 206 <211> LENGTH: 18
 207 <212> TYPE: PRT
 208 <213> ORGANISM: Mycobacterium aurum
 210 <220> FEATURE:
 211 <223> OTHER INFORMATION: SC-S423
 213 <220> FEATURE:
 214 <221> NAME/KEY: UNSURE
 215 <222> LOCATION: (4)
 217 <220> FEATURE:
 218 <221> NAME/KEY: UNSURE
 219 <222> LOCATION: (9)
 221 <400> SEQUENCE: 3
 W--> 222 Thr Ala Leu Xaa Asp Leu Gly Thr Xaa Asn Leu Val Ala Val Glu Pro
 223 1 5 10 15
 225 Gly Ala
 228 <210> SEQ ID NO: 4
 229 <211> LENGTH: 17
 230 <212> TYPE: PRT
 231 <213> ORGANISM: Mycobacterium aurum
 233 <220> FEATURE:
 234 <223> OTHER INFORMATION: SC-S423
 236 <400> SEQUENCE: 4
 237 Ile Ser Ile Phe Asp Thr Gly Phe Gly Ala Ser Asp Leu Thr Tyr Thr
 238 1 5 10 15
 240 Val
 243 <210> SEQ ID NO: 5
 244 <211> LENGTH: 19
 245 <212> TYPE: PRT
 246 <213> ORGANISM: Mycobacterium aurum
 248 <220> FEATURE:
 249 <223> OTHER INFORMATION: SC-S423
 251 <400> SEQUENCE: 5
 252 Asp Arg Phe Trp His Leu Met Asp Glu Pro Gly Pro Leu Ile Glu Thr
 253 1 5 10 15
 255 Ile Glu Tyr
 259 <210> SEQ ID NO: 6
 260 <211> LENGTH: 38
 261 <212> TYPE: DNA
 262 <213> ORGANISM: Artificial Sequence
 264 <220> FEATURE:
 265 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 267 <220> FEATURE:
 268 <221> NAME/KEY: modified_base
 269 <222> LOCATION: (12)
 270 <223> OTHER INFORMATION: i
 272 <220> FEATURE:
 273 <221> NAME/KEY: modified_base
 274 <222> LOCATION: (18)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/067,291

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Input Set : N:\Crf3\RULE60\10067291.txt

Output Set: N:\CRF3\02252002\J067291.raw

275 <223> OTHER INFORMATION: i
 277 <400> SEQUENCE: 6
 W--> 278 ttgagacsg gnttcgngc stcsgaycts acstayac 38
 281 <210> SEQ ID NO: 7
 282 <211> LENGTH: 32
 283 <212> TYPE: DNA
 284 <213> ORGANISM: Artificial Sequence
 286 <220> FEATURE:
 287 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 289 <400> SEQUENCE: 7
 290 ccsggctcgt ccatsagrtg ccagaascgr tc 32
 293 <210> SEQ ID NO: 8
 294 <211> LENGTH: 17
 295 <212> TYPE: DNA
 296 <213> ORGANISM: Artificial Sequence
 298 <220> FEATURE:
 299 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 301 <400> SEQUENCE: 8
 302 gagccggaag atgttg 17
 305 <210> SEQ ID NO: 9
 306 <211> LENGTH: 24
 307 <212> TYPE: DNA
 308 <213> ORGANISM: Artificial Sequence
 310 <220> FEATURE:
 311 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 313 <400> SEQUENCE: 9
 314 ccaccctgcg cgacgtcacc agcc 24
 317 <210> SEQ ID NO: 10
 318 <211> LENGTH: 24
 319 <212> TYPE: DNA
 320 <213> ORGANISM: Artificial Sequence
 322 <220> FEATURE:
 323 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 325 <400> SEQUENCE: 10
 326 tctacgacgc cgacgagttg atgg 24
 329 <210> SEQ ID NO: 11
 330 <211> LENGTH: 32
 331 <212> TYPE: DNA
 332 <213> ORGANISM: Artificial Sequence
 334 <220> FEATURE:
 335 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 337 <400> SEQUENCE: 11
 338 tgccatggct gctctttcag acctcggcac ct 32
 341 <210> SEQ ID NO: 12
 342 <211> LENGTH: 32
 343 <212> TYPE: DNA
 344 <213> ORGANISM: Artificial Sequence
 346 <220> FEATURE:
 347 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/067,291

DATE: 02/25/2002

TIME: 11:54:04

Input Set : N:\Crf3\RULE60\10067291.txt

Output Set: N:\CRF3\02252002\J067291.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6